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Morphological Characterization of Local and Exotic Hot Pepper (*Capsicum annuum* L.) Collections in Uganda

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ABSTRACT

Thirty-seven local and introduced genotypes of hot pepper (*Capsicum annuum*) were characterized for 20 quantitative and 28 qualitative morphological characters under screen-house conditions. There were highly significant differences among genotypes for most quantitative characters ($P<0.001$) except primary branch numbers ($P>0.05$). Exotic genotypes were superior in most traits compared to local genotypes. Local genotypes were characterized by small fruits, late maturity, taller plants with wider canopies compared to introduced genotypes. Local genotypes #31 and #26 were outstanding with respect to numbers of fruits per plant (mean 62) and earliness (60 days), respectively. The first and second principal components (PCs) for quantitative traits accounted for 41.6% and 13.8% of the total variability, respectively. Fruit length, fruit weight and fruit wall thickness largely contributed to PC1. Days to flowering, fruiting, fruit maturity; stem diameter and height; plant height and width largely contributed to PC2. Moderate diversity based on qualitative traits (Mean diversity index H` = 0.53) was detected among genotypes. Higher diversity indices were observed for stem pubescence type (1.16), leaf pubescence type and density (1.02), anther colour (0.94), calyx margin and fruit surface (1.06), and immature fruit colour intensity (1.03). Cluster analyses using 20 quantitative and 28 qualitative traits showed diversity among the genotypes at phenotypic level but with some level of genotypic relatedness and closeness. Based on Euclidean distance in cluster analysis dendrograms, exotic genotypes grouped more with local genotypes in qualitative compared with quantitative traits. The diversity among the germplasm in both qualitative and quantitative traits revealed by this study can be used for trait improvement through selection and gene introgression.

Keywords: diversity index, germplasm, principal component analysis, morphological markers, *Capsicum* breeding

INTRODUCTION

Productivity of pepper in Uganda is mainly affected by pests and diseases. Major diseases include: *Phytophthora* root rot, wilts (IPM CRSP 2011), *Cercospora* leaf spot, viral diseases and anthracnose (Nsabiyera *et al*. 2012). Important pests include: aphids, thrips (Karungi *et al*. 2010), mites and bollworm (Buyinza and Mugagga 2010). In order to manage these pests and diseases farmers rely heavily on and often abuse pesticides (IPM CRSP 2011) whereas host resistance has been reported to be the most cost effective control strategy for farmers (Duveiller *et al*. 2007). Improved pepper varieties are not readily available for commercial production in Uganda and farmers depend on farm-saved seed (Buyinza and Mugagga 2010) which has been reported to be infected with seed-borne pathogens such as viruses (IPM CRSP 2008), bacteria and fungi (Ochwo-Ssemakula, unpublished). The type of hot pepper fruit from Uganda preferred by the international market in Uganda is pungent, disease and pest-free; and possesses big fruit that is red or orange at maturity (Mr. James Kanyije, 2010; pers. comm.). A breeding program for hot pepper is, therefore, necessary in Uganda with the mandate to develop and make available improved varieties with enhanced productivity and pest/disease resistance to farmers. This study was undertaken to characterize morphological traits among local and improved exotic pepper accessions with the aim of identifying the existing diversity for use in *Capsicum* improvement in Uganda.

MATERIALS AND METHODS

Experimental site

A screen-house trial was established at the National Agricultural Research Laboratories Institute (NARL) from March to August 2010. The Institute is located 15 km north of Kampala in Kyadondo county, Wakiso district and stands at an elevation of 1,200 m above sea level. The area has sub-humid climate and receives mean annual precipitation of 1250 mm that has a bimodal distribution. Mean maximum air temperatures vary between 25 and 27°C while minimum temperatures range between 15 and 17°C.

Plant materials and experimental design

Thirty seven (37) hot pepper genotypes were characterized in this study, including 10 local accessions and 27 exotic introductions (mostly from the AVRDC) (**Table 1**). Almost all the local genotypes (10) were collected from farmer's homesteads in three major hot pepper growing districts in Uganda (Wakiso, Kisoro, Kasese) (UEPB 2005). The local varieties were coded by the name of the species, year of collection and a collection number (**Table 1**). One genotype, CA-UGCE 09-3 was collected from ICEMARK-Mashamba field, a local company that exports fresh fruits and vegetables from Uganda. Seeds were extracted and soaked in 10% (w/v) trisodium phosphate (TSP) solution for 2 h 30 min and

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Table 1 Codes and source of hot pepper genotypes characterized for morphological traits in Uganda.

Genotype No.	Code	Source	Origin
1	PBC 375	AVRDC	Taiwan
2	PBC 535	AVRDC	Taiwan
3	PP97-7195-1	AVRDC	Taiwan
4	PP9848-4996	AVRDC	Taiwan
5	PP9852-110	AVRDC	Taiwan
6	PP9852-149	AVRDC	Taiwan
7	PP9852-173	AVRDC	Taiwan
8	PP9955-15	AVRDC	Taiwan
9	PP0007-2247	AVRDC	Taiwan
10	PP0007-2259	AVRDC	Taiwan
11	PP0007-2269	AVRDC	Taiwan
12	PP0042-17	AVRDC	Taiwan
13	PP0237-7502	AVRDC	Taiwan
14	PP0237-7508	AVRDC	Taiwan
15	PP0337-7065	AVRDC	Taiwan
16	PP0337-7545	AVRDC	Taiwan
17	PP0337-7546	AVRDC	Taiwan
18	PP0337-7562	AVRDC	Taiwan
19	PP0437-7506	AVRDC	Taiwan
20	PP0537-7513	AVRDC	Taiwan
21	PP0537-7528	AVRDC	Taiwan
22	PP0537-7539	AVRDC	Taiwan
23	PP0537-7541	AVRDC	Taiwan
24	PP0537-7558	AVRDC	Taiwan
25	PP0537-7504	AVRDC	Taiwan
26	CA-EASC-09-1	EASC[a]	Taiwan
27	CA-PPCHI-08-1	Horticulture Programme	Seed company, China
28	PP9852-115	AVRDC-RCA	Arusha, Tanzania
29	CA-UGKI 09-6[b]	Farmer's homestead	Kisoro, Uganda
30	CA-UGKI 09-5	Farmer's homestead	Kisoro, Uganda
31	CA-UGCE 09-3[c]	ICEMARK (Commercial Field)	Wakiso, Uganda
32	CA-UGKA 09-3	Farmer's homestead	Kasese, Uganda
33	CA-UGKI 09-1	Farmer's homestead	Kisoro, Uganda
34	CA-UGKI 09-2	Farmer's homestead	Kisoro, Uganda
35	CA-UGKI 09-4	Farmer's homestead	Kisoro, Uganda
36	CA-UGKI 09-7	Farmer's homestead	Kisoro, Uganda
37	CA-UGKA 09-4	Farmer's homestead	Kasese, Uganda

[a]East African Seed Company, Kampala
[b]Locally collected genotypes were arbitrary designated names based on the place of origin with prefixes "CE", "KI", "KA", EASC
[c]Commercial variety (ICEMARK, Kampala, Uganda)

Table 1 Descriptors of quantitative morphological traits used to characterize hot pepper in Uganda

Parameter	Descriptors
(PHT) Plant height (cm)	Recorded when 50% of the plants the first fruit has began to ripen
(PWD) Plant canopy width (cm)	Measured immediately after first harvest, at the widest point
(SHT) Stem length (cm)	Height to first bifurcation. Measured immediately after first harvest
(STD) Stem diameter (cm)	measured in the middle part to first bifurcation (10 cm from ground), at mature stage
(PBN) Primary branch numbers	Counted at plant maturity
(SBN) Secondary branch numbers	Counted at plant maturity
(DFL) Days to flowering	Number of days from transplanting until 50% of plants have at least one open flower
(CL) Corolla length (cm)	Average of 10 petals of dissected corolla
(AL) Anther length (mm)	Average anther length of ten representative flowers selected from different plants. Observed immediately at anthesis
(DFR) Days to fruiting	Number of days from transplanting until 50% of the plants bear fruits of about 2 cm in length at the first and second bifurcation
(DFM) Days to fruit maturity	Numbers of days from transplanting until 50% of the plants bear mature fruits at the first and second bifurcation.
(FL) Fruit length (cm)	Average fruit length of 10 ripe fruits of the second harvest
(FW) Fruit width (cm)	Average fruit width of 10 ripe fruits of the second harvest measured at the widest point
(FRTWT) Fruit weight (g)	Average fruit weight of 10 ripe fruits of the second harvest
(FPL) Fruit pedicel length (cm)	Average length of 10 pedicels of the second harvest to one decimal place
(FRWTH) Fruit wall thickness (mm)	Average of 10 ripe fruits of the second harvest, measured at point of maximum width to one decimal Point
(NFP) Number of fruit per plant	Fruit harvests for the duration of the experiment
(NSF) Number of seeds per fruit	Averaged over 10 fruits per plot in a replication
(SD) Seed diameter (mm)	The maximum diameter of 10 seeds to two decimal places
(SWT) Seed weight (g)	Weight of 300 dry seeds.

rinsed in running water for 45 min. Seed were then soaked in water for 24 h in order to facilitate germination (Rashid *et al*. 2007). Single seedlings were transplanted into 5-l buckets 45 days after planting. The buckets were used to establish a randomized complete block design (RCBD) with two replicates. Each replicate had 5 plots at a spacing of 45 cm within rows and 60 cm between rows, with each plot comprising one genotype.

Management of the experiment

Nitrogen-Phosphorus-Potassium (NPK) fertilizer (20:10:10) was applied at a rate of 400 kg/ha in two splits (200 kg/ha two weeks

Table 2 Descriptors of qualitative morphological traits used to characterize hot pepper in Uganda.

Parameter	Descriptors
(NA) Nodal anthocyanin (whole plant) at plant maturity	1: Green, 3: Light-purple, 5: Purple, 7: Dark-purple
(SPT) Stem pubescence type: Recorded on mature plants, at two nodes below the shoot when first fruit turning red.	0: Absent, 3: Short, 5: Intermediate, 7: Long
(SPD) Stem pubescence density: Recorded on mature plants, excluding the first two nodes below the shoot	0: Glabrous, 3: Sparse, 5: Intermediate, 7: Dense
(PGH) Plant growth habit: Observed when 50% of the plants bear ripe fruits	3: Prostate, 5: Intermediate (compact), 7: Erect, 9: Other (specify)
(LS) Leaf shape	1: Deltoid, 2: Ovate, 3: Lanceolate
(LM) Lamina margin	1: Entire, 2: Undulate, 3: Ciliate
(LSF) Leaf surface	1: Smooth, 2: Intermediate, 3: Rough
(LPT) Leaf pubescence type: Observed on the youngest mature leaves when first fruit matures	0: Absent, 3: Short, 5: Intermediate, 7: Long
(LP) Leaf pubescence: Observed on the youngest mature leaves when first fruit matures	0: Glabrous, 3: Sparse, 5: Intermediate, 7: Dense
(PP) Pedicel position: Recorded at anthesis	3: Pendant, 5: Intermediate, 7: Erect
(CC) Corolla colour	1: White, 2: Light-yellow, 3: Yellow, 4: Yellow-green, 5: Purple with white base, 6: White with purple base, 7: White with purple margin, 8: Purple, 9: Other (specify)
STC (Style colour)	1: White, 2: Yellow, 3: Green, 4: Blue, 5: Purple, 6: Other (specify)
(AC) Anther colour: Observed immediately after blooming before anthesis	1: White, 2: Yellow, 3: Pale-blue, 4: Blue, 5: Purple, 6: Other (specify)
(SE) Stigma exsertion in relation to anthers at full anthesis. Average of 10 stigmas from representative flowers selected from each plant per plot	3: Inserted, 5: Same level, 7: Exserted
(CM) Calyx margin	1: Entire, 2: Intermediate, 3: Dentate, 4: Other (specify)
(CAC) Calyx annular constriction: At junction of calyx and pedicel. Observed at mature stage	0: Absent, 1: Present
(AS/S) Anthocyanin spots or stripes: Recorded just before the ripening stage	0: Absent, 1: Present
(IFC) Fruit colour at intermediate stage: Recorded on fruits just before the ripening stage	1: White, 2: Yellow, 3: Green, 4: Orange, 5: Purple, 6: Deep purple, 7: Others (specify)
(IFCI) Intermediate fruit colour intensity: Recorded on fruits just before the ripening stage	3: Light, 5: Medium, 7: Dense, X: Mixture
(MFC) Fruit colour at mature stage	1: White, 2: Lemon-yellow, 3: Pale orange-yellow, 4: Orange-yellow, 5: Pale orange, 6: Orange, 7: Light red, 8: Red, 9: Dark red, 10: Purple, 11: Brown, 12: Black, 13: Others (specify)
(MFCI) Mature fruit colour intensity: Recorded on fruits at maturity	3: Light, 5: Medium, 7: Dense, X: Mixture
(FS) Fruit shape	1: Elongate, 2: Almost round, 3: Triangular, 4: Campanulate, 5: Blocky, 6: Other (specify)
(FSP) Fruit shape at pedicel attachment	1: Acute, 2: Obtuse, 3: Truncate, 4: Cordate, 5: Lobate
(FN) Neck at base of fruit	0: Absent, 1: Present
(FSB) Fruit shape at blossom end: Average of 10 fruits	1: Pointed, 2: Blunt, 3: Sunken, 4: Sunken and pointed, 5: Other (specify) 0: Absent, 1: Present
(FXC) Fruit cross-sectional corrugation: Average of 10 fruits (1/3 from pedicel end)	3: Slightly corrugated, 5: Intermediate, 7: Corrugated
(FS) Fruit surface	1: Smooth, 3: Semi-wrinkled, 3: Wrinkled

after transplanting and 200 kg/ha three weeks after the first application). Urea was applied at the rate of 100 kg N/ha in three splits: 30 kg N/ha two weeks after transplanting, 30 kg N/ha three weeks after the first application and 40 kg N/ha three weeks after the second application. Ridomil (Syngenta Crop Protection AG, Basle, Switzerland) [Metalaxyl-M 40 g/kg, Mancozeb 640 g/kg active ingredient (ai)] was applied once (rate 60 g/15 l) to control fungal infection. Tafgor (Rallis India Ltd, Mumbai, India) 40 EC (Dimethoate 40% EC ai, rate 30 ml/15 l) and Alfapor spray and dip (Alfasan International BV, Ja Woerden, Holland) (50 mg/ml α-cypermethrin EC, rate 15 ml/15 l) were applied interchangeably to protect against insect pests and vectors of viral diseases. Weeding was done twice a month and plants watered twice a day for the duration of the experiment. At flowering, plants were trained using sisal strings to provide a grid of support.

Data recording

Data were recorded on 20 quantitative (**Table 2**) and 28 qualitative (**Table 3**) morphological characters, covering the vegetative parts of the plant, inflorescence, fruit and seed in a protocol adapted from IPGRI *et al*. (1995) and Engle (2001). For quantitative characters, data were collected on all the five plants in a replicate and the mean values considered. Qualitative descriptors were scored on all 10 plants per genotype in the experiment.

Data analyses

Quantitative data were subjected to Analysis of Variance (ANOVA) using GenStat computer package (12th edition, Version 12.2; VSN International Ltd. 2010). Two multivariate analysis methods were used, principal component analysis (PCA) and hierarchical cluster analysis. Mean values of all quantitative traits were standardized so as to assume values from the same interval according to Kalbarczyk (2010) as follows:

$$Z_i = [X_i - Min\ (X_i)]/[Max\ (X_i) - Min\ (X_i)]$$

where:
Min (X_i): Lowest value of the ith factor
Max (X_i): Highest value of the ith factor

Standardized trait values were subjected to principal coponent analysis (PCA) using the appropriate options of the XLSTAT statistical computer package (Version 2011.3.01) to determine the traits most effective in discriminating between genotypes basing on Pearson (n-1) Correlation Coefficients Matrix procedure generated by the package. Principal components coefficients, eigenvalues, and relative and cumulative proportions of the total variance expressed by single traits were calculated. Principal components with eigenvalues >1 were extracted for interpretation as recommended (Kaiser 1960; Anonymous 2010; Wuensch 2010). The first two components explaining the maximum variance were rotated by Varimax method for uncorrelated components with

Table 4 Analysis of variance, mean and range of quantitative traits of 37 hot pepper genotypes characterized in the screen house at NARL in Uganda from 2009-2010.

Parameter	Genotype (df =36)	Genotypic means				LSD (0.05)	CV (%)
	Mean Squares × 10^2	Local	Exotic	Grand	Range		
Days to flowering (days)	20174.00***	44.3	36.7	41.7	14.0-60.5	10.93	12.9
Days to fruiting (days)	18430.00**	47.9	40.1	46.1	19.5-65.0	17.09	18.3
Days to fruit maturity (days)	22990.00***	93.5	86.0	90.8	58.5-108.5	15.84	8.6
Number of fruit per plant	9564.00***	20.3	11.9	13.0	4.0-44.5	9.55	36.3
Fruit length (cm)	2879.00***	5.1	11.3	9.4	2.2-16.1	2.65	13.9
Fruit width (cm)	30.20***	1.5	1.7	1.7	0.96-3.0	0.30	8.7
Fruit pedicel length (cm)	92.00***	3.4	3.5	3.4	2.3-5.1	0.71	10.4
Fruit wall thickness (mm)	5.57***	1.0	3.0	1.7	0.8-3.0	0.07	19.6
300 seed weight (g)	10.60***	1.5	1.6	1.6	1.1-2.0	0.20	6.4
Number of seeds per fruit	114790.00***	57.1	74.3	71.7	31.1-149.1	22.66	15.6
Stem diameter (mm)	69.00***	13	11	11	7.0-13	0.23	10.9
Stem height (cm)	20194.00***	34.0	25.7	27.0	6.7-55.0	7.20	13.1
Primary branch numbers	2.20^{ns}	2.1	2.1	2.1	2.0-2.4	0.31	7.3
Secondary branch numbers	589.40***	8.6	5.8	6.0	4.0-9.8	1.75	14.3
Plant width (cm)	35303.00***	84.2	68.8	69.4	44.1-108.5	12.91	9.2
Plant height (cm)	67723.00***	99.6	75.1	78.9	47.1-129.1	15.02	9.4
Seed diameter (mm)	3.53***	4.0	4.0	4.0	3.0-5.0	0.05	6.9
Fruit weight (g)	10521.00***	3.0	10.9	8.7	1.2-37.4	3.91	22.2
Corolla length (mm)	178.0***	13	12	12	5.0-18	0.07	2.8
Anther length (mm)	4.52***	3.0	3.0	3.0	2.0-4.0	0.01	1.8

Kaiser Normalization, and plotted together to generate a trait and genotype bi-plot for ease of interpretation of variables that load on more than one component (Anonymous 2010; Wuensch 2010). Euclidean distance (Coefficient of similarity) was estimated to generate a matrix for assessing level of dissimilarity between genotypes using cluster analysis on both quantitative and qualitative traits based on the Complete Link method of the GenStat computer package (12^{th} edition, Version 12.2; VSN International Ltd. 2010). The generated phenograms were used to determine clusters with high similarity coefficients. The phenotypic diversity among genotypes by qualitative traits was further assessed using Shannon-Weaver diversity index (Shannon and Weaver 1949), calculated based on phenotypic frequency of alleles controlling each qualitative trait category of descriptors as follows:

$$H' = -\sum_{i=1}^{S}(p_i \ln p_i)$$

$$H' = \blacksquare \sum_{i=1}^{S}(p_i \ln p_i)$$

where:
H′: Diversity index
S: Total number of descriptor states in the i-th descriptor
P_i: Fraction of individuals belonging to the i-th descriptor state (number of observations/descriptor state in the i-th descriptor divided by the total number of characterized plants.

RESULTS

Analysis of quantitative morphological traits

1. Analysis of variability in quantitative morphological traits among hot pepper genotypes

Analysis of variance showed highly significant variability among genotypes in 19 traits ($P<0.01$ for days to fruiting, and $P<0.001$ for the rest of traits), except number of primary branches ($P=0.579$) (**Table 4**). In general, the local genotypes were taller, matured later, had smaller fruit size and produced lower yields compared to the improved exotic genotypes, except for the East African seed company genotype 26 that was the earliest maturing, was shorter and produced medium fruit size genotype (**Table 5**). The AVRDC genotypes 8, 19 and 16 and the Chinese seed company genotypes 27 had the largest fruits. However, genotype 27 was shorter and yielded fewer fruits per plant (**Table 5**).

2. Principal component analysis of quantitative traits

Principal component analysis grouped the 20 quantitative traits into 20 principal components (data not shown). The first 4 PCs had Eigen values distinctly above 1 (8.3, 2.8, 1.7 and 1.5, respectively) (**Table 6**) and were therefore examined further (Kaiser 1960; Anonymous 2010; Wuensch 2010). The four components together accounted for 71.18% of the total variability with the first two components accounting for 55.4% of the total variance and hence were the most meaningful components (**Table 6**). A given trait was considered an important contributor to the variability in a component if its vector loading had an absolute value ≥ 0.40 for that component and < 0.40 for the other components (Anonymous 2010; Wuensch 2010). Based on this measure, high positive loadings that accounted for variability on the first PC in the descending order were: fruit length, fruit weight, fruit wall thickness, fruit width, number of seeds per fruit, seed diameter, 300 seed weight and anther length while those that contributed negatively in the descending order were plant height, stem diameter, plant width, day to flowering, stem height, days to fruiting, number of fruits per plant, days to fruit maturity, secondary branch numbers. The high positive loadings in decreasing order of importance were of days to flowering, days to fruiting, days to fruit maturity, fruit width, fruit wall thickness, primary branch numbers, fruit weight account for more variability on PC2. Three high positive loadings of corolla color, anther length, number of seeds per fruit and 300 seed weight contributed most on variability of PC3. Two high positive loadings of fruit pedicel length and secondary branch numbers and one high negative loading of primary branch numbers contributed most to the variability on fourth PC.

In the four extracted principal components, many variables load on more than one component making interpretation difficult since they seemed to measure similar constructs. Varimax rotation with Kaiser Normalization of the first two components explaining the greatest variance of total variance eased interpretation. Results of the rotation indicate that the first two PCs account for 55.4% of the total variance with PC1 contributing 28.16% and PC2 27.23% (**Table 6**). Both fruit length and plant width load on both components with loadings above 0.4, and are dropped from interpretation since they are not pure measures of any one construct (Anonymous 2010). Consequently, the meaningful positive loadings for PC1 after Varimax rotation in the

Table 5 Means for 20 quantitative characters of 37 *Capsicum annuum* L. genotypes characterized under screen house conditions at NARL in Uganda during 2009-2010.

Variety	DFL (days)	DFR (days)	DFM (Days)	NFP (fruits)	FL (cm)	FW (cm)	FPL (cm)	FRWTH (mm)	FRTWT (g)	NSF	300SWT (g)	SD (mm)	STD (mm)	SHT (cm)	PBN	SBN	PWD	PHT	CL (mm)	AL (mm)
1	28	33	82	12	9.3	1.8	3.5	1.7	7.8	61	1.7	4	9.8	26.0	2.0	8.0	78	68	12.7	3.0
2	38	41	91	8	11.5	2.0	2.6	1.7	10.8	72	1.8	4	9.5	17.3	2.0	4.0	68	72	11.9	3.0
3	51	55	92	11	9.7	1.7	3.6	1.9	7.4	70	1.6	3	13.0	21.5	2.0	5.8	66	86	14.4	3.0
4	34	38	78	21	9.1	1.3	3.7	1.1	3.0	61	1.7	4	10.8	31.1	2.0	9.5	87	84	11.0	3.0
5	47	50	94	21	5.6	1.3	2.9	1.1	2.8	50	1.8	4	12.3	33.8	2.0	9.8	66	76	12.1	3.0
6	44	48	93	14	12.6	1.8	3.2	1.8	9.6	70	1.6	4	14.5	36.8	2.0	5.3	79	92	12.0	3.0
7	45	48	91	12	8.6	1.5	3.2	1.6	8.3	62	1.6	4	10.8	27.3	2.5	5.5	77	97	8.5	3.0
8	33	36	78	12	15.2	2.0	3.8	2.4	22.9	148	1.5	4	9.5	23.3	2.2	5.8	67	65	17.2	4.0
9	24	28	82	7	9.0	1.6	2.7	1.9	6.5	64	1.6	4	10.3	21.1	2.0	4.3	70	78	12.7	3.0
10	28	31	85	11	11.2	1.7	3.0	1.8	9.0	80	1.7	3	9.0	21.0	2.2	4.8	63	75	5.3	3.0
11	28	31	78	13	12.6	1.9	5.3	2.3	5.9	51	1.5	4	9.0	26.8	2.0	7.5	62	62	6.0	4.0
12	41	42	95	23	11.3	1.6	4.0	1.8	6.6	40	1.6	4	11.0	37.7	2.5	6.5	69	70	11.9	2.2
13	31	35	80	7	11.6	1.5	2.6	1.6	7.9	81	1.4	4	9.5	21.4	2.0	4.0	71	82	9.7	3.0
14	55	59	103	12	10.6	1.4	3.5	1.8	7.2	58	1.7	4	11.5	16.6	2.0	4.5	70	86	12.0	3.0
15	23	26	71	18	11.3	1.5	3.5	1.6	8.5	102	1.3	4	8.0	23.0	2.0	6.8	50	49	11.4	3.0
16	33	35	77	8	12.3	2.1	3.4	3.9	18.3	101	1.6	4	10.5	19.9	2.0	4.0	72	61	16.0	4.0
17	33	36	89	10	10.1	1.8	2.6	1.8	7.9	64	1.8	4	12.8	24.2	2.0	4.3	83	81	10.1	3.0
18	46	50	93	11	14.0	2.0	5.3	2.1	15.0	69	1.5	4	11.8	29.4	2.0	4.8	73	95	15.2	3.0
19	49	52	94	7	14.9	2.3	3.3	2.8	20.9	72	1.9	4	10.5	24.2	2.0	4.3	62	77	9.7	2.4
20	41	46	91	16	6.7	1.4	2.5	1.5	3.7	59	1.4	4	10.0	27.4	2.0	5.3	73	90	11.3	2.0
21	23	27	73	14	12.7	1.4	2.9	1.7	9.2	82	1.5	4	7.5	25.0	2.0	6.0	66	69	10.0	3.0
22	35	39	82	8	12.0	1.5	3.4	2.1	9.8	57	1.6	4	9.3	25.3	2.0	4.0	58	59	7.7	3.0
23	44	48	100	11	13.3	1.8	3.7	2.0	11.8	60	1.2	4	12.5	23.9	2.2	4.5	58	72	16.3	3.0
24	37	40	84	9	10.2	2.0	4.7	1.8	12.7	63	2.0	4	12.3	31.8	2.0	8.0	82	84	10.5	3.0
25	35	39	82	16	8.8	1.2	3.5	1.2	4.9	62	1.3	3	11.3	34.6	2.0	7.0	90	77	12.3	3.9
26	10	13	60	15	9.7	1.5	2.9	1.5	4.6	45	2.0	4	11.5	22.9	2.0	6.5	56	66	13.1	3.0
27	37	41	83	4	16.9	3.1	3.9	2.7	44.4	133	1.9	4	9.5	23.8	2.0	4.5	56	62	11.2	4.0
28	27	30	80	5	14.7	1.9	3.5	2.0	12.5	115	1.9	5	7.3	20.0	2.2	5.0	42	58	12.5	3.7
29	48	52	94	22	3.2	2.0	2.6	1.6	2.7	70	1.5	3	12.7	27.1	2.0	9.3	79	94	16.2	3.0
30	51	56	101	13	3.6	2.0	4.0	1.4	3.4	70	1.3	3	12.8	54.2	2.0	8.3	87	105	12.9	3.0
31	46	50	101	62	4.7	1.0	3.2	1.0	1.5	31	1.2	4	13.0	36.9	2.0	10.5	85	90	11.3	3.0
32	31	34	75	11	11.2	1.3	3.3	1.4	4.0	51	1.8	5	7.8	8.2	2.3	6.5	56	55	13.5	2.9
33	45	48	93	12	6.1	1.6	5.5	1.7	5.4	48	1.8	4	10.8	24.2	2.0	7.5	82	110	11.6	3.0
34	47	51	95	14	4.1	1.5	3.6	1.1	3.1	59	1.4	4	14.8	46.1	2.2	10.3	119	124	7.7	2.0
35	59	63	112	18	2.8	1.2	3.3	2.1	1.3	55	1.4	4	14.0	50.9	2.2	6.5	93	136	8.0	3.0
36	51	53	99	15	2.2	1.6	3.0	1.3	2.8	77	1.4	3	13.0	24.5	2.2	10.3	84	90	16.0	3.0
37	55	59	105	21	3.5	0.9	2.4	0.9	1.3	65	1.1	4	14.3	45.3	2.5	8.9	99	125	17.9	3.0

DFL: Days to flowering, DFR: Days to fruiting, DFM: Days to fruit maturity, FL: Fruit length, FW: Fruit Width, FPL: Fruit pedicel length, FRWTH: Fruit wall thickness, 300 SWT: 300 seed weight, NSF: Number of seeds per fruit, NFP: Number of fruit per plant, SHT: Stem height, SBN: Secondary branch numbers, PBN: Primary branch numbers, PWD: Plant width, PHT: Plant height, SD: Seed diameter, FRTWT: Fruit weight, CL: Corolla length, AL: Anther length, STD: Stem diameter

descending order are fruit weight, fruit width, fruit wall thickness, number of seeds per fruit, 300 seed weight and seed diameter while meaningful negative loadings were number of fruits per plant and secondary branch numbers. This component is thus related to yield traits whose genotypes with big fruits and seeds, few numbers of secondary branch numbers and fruits per plant contributed more to its variability. The meaningful traits that loaded highly on PC2 in descending order were positive values of days to flowering, days to fruit maturity, days to fruiting, plant height, stem diameter, stem height and plant width which are related to growth traits. Genotypes with late maturity, taller plants and wider canopies contributed more to the variability of this component.

In the bi-plot genotypes clustered according to similarity, regardless of source. Genotypes on the negative side of horizontal axis (PC1) had small fruits and seeds, many primary branch numbers and number of fruits per plant while genotypes on the positive side had big fruits and seeds, few primary branch numbers and number of fruits per plant. Genotypes on the positive side of vertical axis (PC2) were tall, late-maturing plants with wide canopies and stems while genotypes on the negative side of the vertical axis were short, early-maturing plants with narrow canopies and stems (**Fig. 1**). Apart from the AVRDC genotypes 14 and 8, all the other genotypes clustered into four quadrants I, II, III, IV. Genotypes 14 and 8 shared characteristics of both quadrants between which they fell. Genotypes 31, 20, 36, 29, 33, 37, 34, 30 and 35 grouped in quadrant I of the bi-plot are characterized by late maturity, tall plants with wide plants and stem, small fruits and seeds, many secondary branch numbers and fruits per plant. Genotypes 20, 36, 29 and 33 are intermediate in these traits. The local genotype 35 was the most late maturing, the tallest with widest plant canopies and stems while the local commercial check 31 had the smallest fruits and seeds and most number of fruits and secondary branch numbers. AVRDC genotypes 3, 12, 6, 23, 24, 18 and 19 were separated into quadrant II that typically had late-maturity, tall plant with wide canopies, big stems, big fruits and seeds, few secondary branch numbers and number of fruits per plant. The genotypes in this group exhibited intermediate ranges for these traits except for genotype 19 that had big fruits and seeds, few secondary branch numbers and number of fruits per plant. Genotypes 5, 4, 25, 10, 1, 15, 9, 11, 21, 32 and 26 were classified into quadrant III with early-maturity types that also had small fruits and seeds, many secondary branch numbers and number of fruits per plant. In this quadrant, all genotypes had intermediate traits except the local genotypes 32 and 26 that were the earliest maturing and had short

Table 6 Principal component (PC) analysis of 20 quantitative characters from 37 *C. annuum* L. hot pepper genotypes characterized in the screen house at NARL in Uganda from 2009-2010.

Trait	Eigenvectors (principal components)						
	Before Varimax rotation					After Varimax rotation	
	PC1	PC2	PC3	PC4	PC5	PC1	PC2
Eigen values (variance)	8.328	2.751	1.682	1.475	1.055	5.632	5.447
Proportion of variance (%)	41.64	13.76	8.41	7.37	5.28	28.16	27.23
Cumulative variance (%)	41.64	55.4	63.81	71.18	76.46	28.16	55.39
	Factor loadings (correlation coefficients)						
Days to flowering	-0.712	0.595	-0.011	-0.178	0.032	-0.097	0.923
Days to fruiting	-0.679	0.516	0.002	-0.200	-0.020	-0.129	0.843
Days to fruit maturity	-0.670	0.544	0.022	-0.096	-0.017	-0.103	0.856
Fruit length (cm)	0.872	0.199	-0.068	0.029	0.000	0.765	-0.463
Fruit width (cm)	0.697	0.525	0.089	0.186	-0.180	0.866	-0.107
Fruit pedicel length (cm)	0.226	0.327	-0.080	0.638	0.406	0.390	0.078
Fruit wall thickness (cm)	0.721	0.521	-0.038	-0.010	-0.040	0.880	-0.127
300 seed weight (g)	0.545	0.076	-0.631	0.117	0.072	0.445	-0.324
Average number of seeds per fruit	0.618	0.372	0.437	-0.008	-0.113	0.703	-0.163
Average number of fruits per plant	-0.676	-0.342	0.281	0.090	0.200	-0.724	0.224
Stem diameter (cm)	-0.811	0.278	-0.011	0.232	-0.042	-0.389	0.764
Stem height (cm)	-0.704	0.324	0.009	0.343	-0.070	-0.280	0.723
Secondary branch numbers	-0.625	-0.260	0.185	0.422	0.294	-0.630	0.247
Primary branch numbers	-0.105	0.440	-0.045	-0.490	0.544	0.231	0.390
Plant width (cm)	-0.773	0.149	-0.114	0.315	-0.177	-0.452	0.644
Plant height (cm)	-0.825	0.372	-0.161	0.114	-0.061	-0.335	0.841
Stem diameter (cm)	0.553	0.029	-0.347	0.161	0.496	0.418	-0.364
Average fruit weight (g)	0.762	0.509	0.121	0.122	-0.096	0.901	-0.164
Corolla length (cm)	0.005	0.126	0.641	-0.222	0.343	0.091	0.087
Anther length (cm)	0.491	0.003	0.610	0.370	-0.016	0.355	-0.339

PC1-5: Principal components 1-5

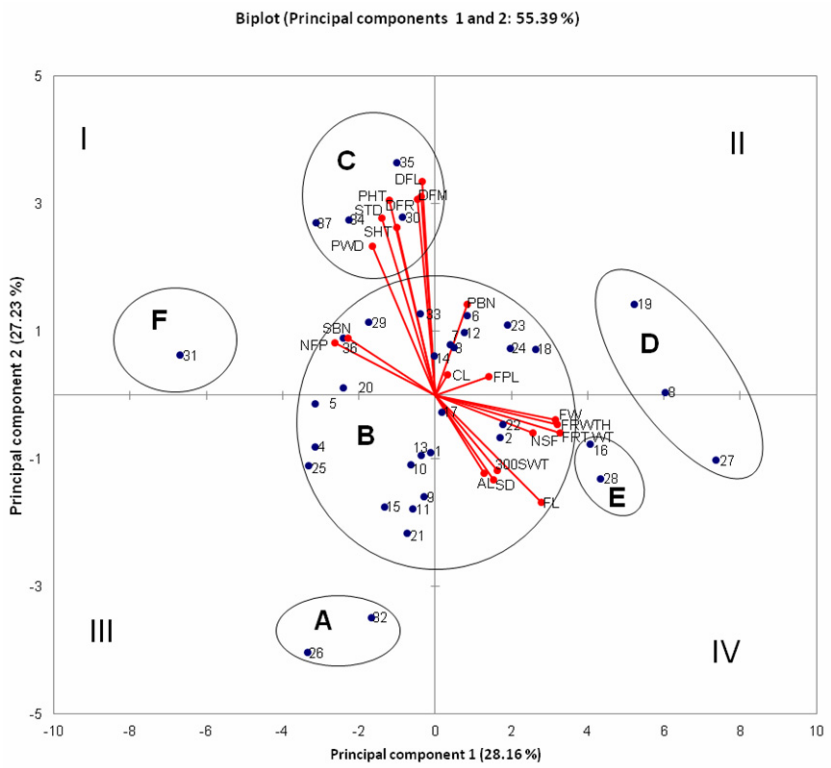

Fig. 1 Bi-plot showing variation of hot pepper accessions by morphological traits based on the 1st and 2nd Principal Component values using 20 quantitative descriptors after Varimax rotation. Figures are genotypes, abbreviated letters are descriptors. Genotypes 1-25, 27-28: Exotic; genotypes 26, 29-37: Local.

plants with narrow canopies and narrow stems that made them susceptible to lodging. Exotic genotypes 17, 22, 2, 16, 28 and 27 clustered in quadrant IV of the bi-plot characterized by early-maturity types that were short and had narrow canopies with narrow stems, big fruits and seeds and few secondary branch numbers and number of fruits per plant. Genotype 27 from the Chinese seed company had the biggest fruits and seeds and the fewest secondary branch numbers and number of fruits per plant compared to the other types in this quadrant.

The bi-plot also grouped genotypes into 6 sub-clusters A-F. Cluster A (26, 32) had negative loadings of PC2, cluster B (with most traits and genotypes) had intermediate loadings of both PC1 and PC2, cluster C (30, 35, 35, 37) had high positive loadings of PC2, cluster D (19, 8, 27) had high positive loadings of PC1, cluster E (16, 28) had intermediate loadings of PC1) while cluster F (31) has high negative loadings of PC1. Genotypes that generally separated most from the rest (26, 32, 35, 19, 8 and 27) were comparatively more diverse and showed potential for use in

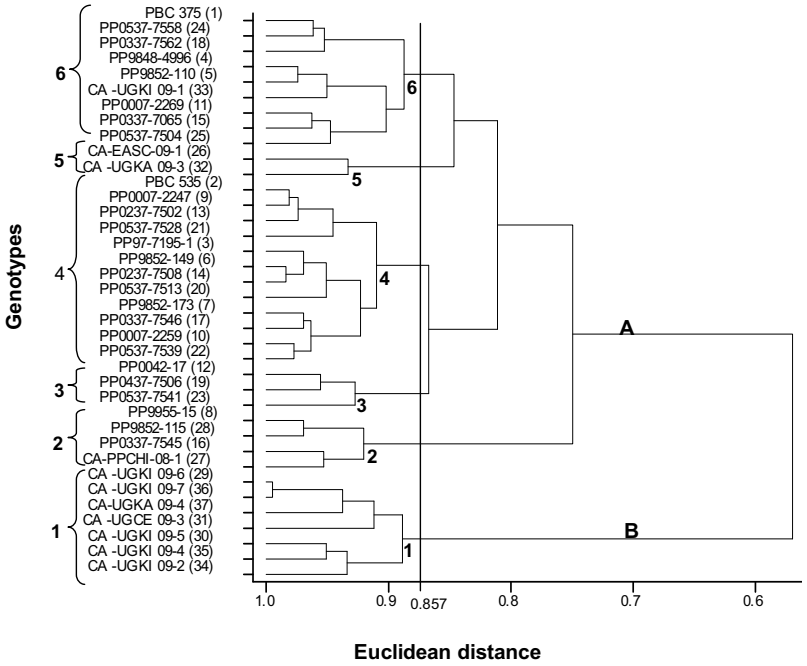

Fig. 2 Dendrogram generated by hierarchical cluster analysis showing the relationships among the characterized hot pepper genotypes using 20 quantitative traits. In brackets are genotype codes. Euclidean Distance = Coefficient of similarity.

Table 7 Percentage distribution of 28 qualitative descriptor traits and their derived diversity indices in *Capsicum annuum* genotypes characterized in a screen house at NARL in Uganda from 2009-2010.

Descriptor trait	Descriptor occurrence frequency (%)				H'
Nodal anthocyanin	Green = 81	Light purple = 11	Purple = 8		0.61
Stem pubescence type	Absent = 22	Short = 54	Intermediate = 8	Long = 16	1.16
Stem pubescence density	Glabrous = 78	Intermediate = 11	Dense = 11		0.67
Plant growth habit	Prostate = 8	Intermediate = 78	Erect = 14		0.67
Leaf surface	Smooth = 76	Intermediate = 11	Rough = 14		0.72
Leaf shape	Ovate = 43	Lanceolate = 57			0.36
Leaf pubescence density	Glabrous = 46	Sparse = 38	Intermediate = 16		1.02
Leaf pubescence type	Absent = 46	Short = 38	Intermediate = 16		1.02
Leaf margin	Entire = 100				0.00
Corolla colour	White = 100				0.00
Anther colour	Pale-blue = 11	Blue = 54	Purple = 35		0.94
Stigma exersion	Inserted = 3	Same = 16	Exerted = 81		0.56
Pedicel position	Pendant = 84	Erect = 16			0.44
Style colour	White = 95	Purple = 5			0.21
Calyx margin	Entire = 22	Intermediate = 38	Dentate = 41		1.06
Calyx annular constriction	Absent = 46	Present = 54			0.69
Anthocyanin spots/stripes	Absent = 89	Present = 11			0.34
Immature fruit colour	Green = 100				0.00
Immature fruit colour intensity	Light = 19	Medium = 49	Dense = 32		1.03
Mature fruit colour	Orange = 5	Red = 95			0.21
Mature fruit colour intensity	Medium = 54	Dense = 46			0.69
Fruit shape	Elongate = 89	Triangular = 11			0.34
Fruit shape at pedicel attachment	Acute = 24	Obtuse = 68	Truncate = 8		0.81
Fruit neck at pedicel attachment	Absent = 100				0.00
Fruit shape at blossom end	Pointed = 95	Blunt = 5			0.21
Fruit blossom end appendage	Absent = 100				0.00
Fruit wall corrugation	Absent = 100				0.00
Fruit surface	Smooth = 38	Semi-wrinkled = 22	Wrinkled = 40		1.06
Mean (H')					0.53

H' = Shannon-Weaver Diversity Index

pepper improvement in their respective superior traits.

3. Hierarchical cluster analysis of quantitative traits

The genotypes were grouped into two major clusters and several sub-clusters (**Fig. 2**). Partitioning clusters at a similarity coefficient of 0.857 for ease of interpretation generated 6 clusters. Cluster 1 contained seven local genotypes with similarity coefficients ranging from 0.889-0.996. Cluster 2 consisted of four exotic genotypes, 3 from AVRDC and one (27) from the Chinese seed company (similarity coefficients ranging from 0.921-0.969). Cluster 3 had three AVRDC genotypes 12, 19 and 23 (similarity coefficients in the range of 0.928-0.957). Cluster 4 was the largest, consisting of 12 genotypes from AVRDC. Similarity coefficients of the genotypes in this cluster varied from 0.867-0.985. Only two local genotypes 26 and 32 constituted cluster 5 (coefficient of similarity of 0.933). There were nine genotypes in cluster 6 with similarity coefficient varying from

0.888 and 0.975. Eight of the genotypes from this cluster were from AVRDC while the remaining genotype (33) was obtained from a local source. The local genotypes 29 and 36 collected from Kisoro and Kasese, respectively were the most similar (similarity coefficient of 0.996). The second most similar genotypes were 6 and 14 from AVRDC (similarity coefficient of 0.985). Of all genotypes that sub-clustered together in a pair, 26 and 32 were the most dissimilar (similarity coefficient of 0.933).

Analysis of morphological qualitative traits

1. Shannon-Weaver diversity index analysis of 28 morphological qualitative traits

Overall, the frequency distributions of 28 qualitative traits shows a wide range of variation, although several traits showed few genotypes that differed from the predominant trait characteristics (**Table 7**). The predominant traits included: entire leaf margin, white corolla colour and medium green immature fruits (100% frequency), white styles, medium red mature fruits and pointed fruits at blossom end (95%), elongate fruits (89%) and pendant pedicel position (84%). The detailed qualitative trait data for various genotypes are shown (**Table 8**). Moderately high diversity was realized with the Shannon-Weaver diversity index (Mean H`= 0.53) although with the index being medium to high for several traits (**Table 7**). The index was high for stem pubescence type (1.16), leaf pubescence density and type (1.02); anther colour (0.94), calyx margin and fruit surface (1.06), and immature fruit colour intensity (1.03). The lowest diversity was recorded in style colour, mature fruit colour and fruit shape at blossom end (0.15) while no diversity was detected among genotypes for leaf margin, corolla colour, immature fruit colour, fruit neck at pedicel attachment, fruit blossom end appendage and fruit wall corrugation traits. All the genotypes had mature red fruit colour apart from local genotypes 29 and 35 that were orange at maturity. Similarly, only AVRDC genotypes 8 and 16 had purple style colour while the rest had white style colours.

2. Hierarchical cluster analysis of 28 morphological qualitative traits

Cluster analysis of qualitative traits grouped genotypes into two major clusters A and B, with coefficients of similarity of 0.698 and 0.605. Major clusters were further sub-divided into 8 sub-clusters, when partitioned at a similarity coefficient of 0.8, for ease of discussion (**Fig. 3**). Genotypes did not cluster together on the basis of the geographical origin. Sub-cluster 3 (at similarity coefficient 0.808) was the largest and contained 12 genotypes, with 17 and 20 being the most similar (at 0.952 similarity coefficient). Cluster 1 (with a similarity coefficient of 0.968) comprised of 7 genotypes including local genotypes 26 and 32 that were the most similar at similarity coefficient of 0.806. Cluster 2 (similarity coefficient of 0.866) had 6 genotypes all from AVRDC, of which 23 and 26 were the most similar at 0.965 similarity coefficient.

Cluster 4 at similarity coefficient of 0.841 has one local genotype and 2 exotic genotypes with local genotype 33 and AVRDC genotype 8 being the most similar at similarity coefficient of 0.929. Each of the clusters 5, 6 and 8 has 2 genotypes at similarity coefficients of 0.829, 0.869 and 0.892, respectively while cluster 7 has 3 local genotypes only at similarity coefficient of 0.837 with 29 and 36 being the most similar at similarity coefficient of 0.864. Like quantitative traits, genotypes 29 and 39 collected from Kisoro and Kasese districts, respectively are the most similar based on qualitative traits. They only differ in 7 of the 28 studied traits including, stem pubescence, stem pubescence density, anther colour, pedicel position, immature fruit colour intensity, mature fruit colour and fruit shape (**Table 8**). Among the introduced genotypes, 22 and 23 were the most similar differing only in 4 of the 28 qualitative traits including; nodal anthocyanin, calyx margin, fruit shape and fruit shape at pedicel attachment (**Table 8**). Of all the two genotypes that clustered together, the local commercial genotype 31 and AVRDC genotype 18 were the most dissimilar with the similarity coefficient of 0.816 (**Fig. 3**). They differ in 11 of the 28 qualitative traits charac-

Table 8 Descriptor scores of 28 qualitative characters of 37 *C. annuum* L. genotypes characterized in the study.

Trait	Genotype																																			
	31	9	17	6	30	33	29	5	2	13	18	28	1	23	12	8	26	15	32	19	7	16	35	21	34	3	20	27	22	4	24	11	10	25	14	36	37
	Scores																																				
NA	1	1	1	1	5	3	3	1	1	1	1	5	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	5	1	1	1	1	3	1
SPT	3	3	3	7	3	3	7	3	5	3	0	0	3	3	3	3	0	3	3	0	3	0	7	0	3	3	5	0	3	3	7	0	3	7	3	5	7
SPD	3	3	3	5	3	3	7	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	7	3	3	3	5	3	3	3	5	3	3	7	3	5	7
PGH	5	5	5	7	7	5	5	5	3	3	7	5	5	5	5	5	5	5	5	5	5	3	7	7	5	5	5	5	5	5	5	5	5	5	5	5	5
LS	1	1	1	1	3	1	1	1	1	1	2	3	1	1	3	1	1	1	2	1	3	1	1	1	1	1	2	1	1	2	3	1	1	1	1	1	1
LSH	3	3	3	3	3	2	3	2	3	2	3	3	2	2	3	2	2	3	2	2	2	3	3	3	3	2	3	2	2	3	2	2	2	3	3	3	3
LP	3	3	0	0	3	0	5	3	3	3	0	3	0	3	3	0	0	0	0	0	0	0	5	0	0	0	0	3	3	0	3	5	5	3	3	5	5
LPT	3	3	0	0	3	0	5	3	3	3	0	3	0	3	3	0	0	0	0	0	0	0	5	0	0	0	0	3	3	0	3	5	5	3	3	5	5
LM	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
AC	4	3	4	3	5	4	5	4	4	4	4	5	3	5	5	5	4	4	5	4	4	5	4	5	4	4	5	4	5	4	5	4	3	5	4	4	4
SE	7	7	5	7	7	7	7	7	7	7	5	5	7	7	5	5	7	7	7	7	7	5	7	7	7	7	7	7	7	7	3	7	7	7	7	7	7
PP	7	3	3	3	3	3	7	7	3	3	3	7	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	7	3	3	3	7	3	3	3
STC	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	5	1	1	1	1	5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CM	3	3	2	2	1	3	1	3	2	2	3	2	3	3	3	3	3	3	3	1	2	2	2	2	1	1	2	3	2	2	1	3	3	1	2	1	2
CAC	0	1	1	1	0	1	1	0	1	1	0	1	1	0	1	1	0	0	0	1	0	1	1	0	1	1	1	1	0	0	0	1	0	0	0	1	0
AS/S	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
IFC	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
IFCI	7	3	7	5	7	5	7	5	5	7	3	7	5	5	7	3	5	3	7	5	5	5	3	7	7	5	5	5	5	7	7	5	3	3	5	5	5
MFC	5	5	5	5	5	5	3	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	3	5	5	5	5	5	5	5	5	5	5	5	5	5	5
MFCI	5	7	7	7	7	5	5	5	5	7	5	7	7	5	7	5	7	7	7	5	5	5	5	5	7	7	7	5	5	7	7	7	5	5	5	5	5
FS	1	1	1	1	3	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1
FSP	2	2	2	2	2	2	3	2	2	2	1	2	2	1	1	2	2	1	2	2	2	2	2	2	2	2	2	3	2	1	2	1	2	1	1	3	1
FN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FSB	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1
FBA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FXC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FS	1	1	1	3	1	5	1	5	3	3	3	5	3	5	1	5	5	5	5	3	1	1	1	5	1	1	1	1	3	5	1	5	3	5	5	5	5

Genotype numbers, see **Table 1**; Trait abbreviations and trait codes, see **Table 3**

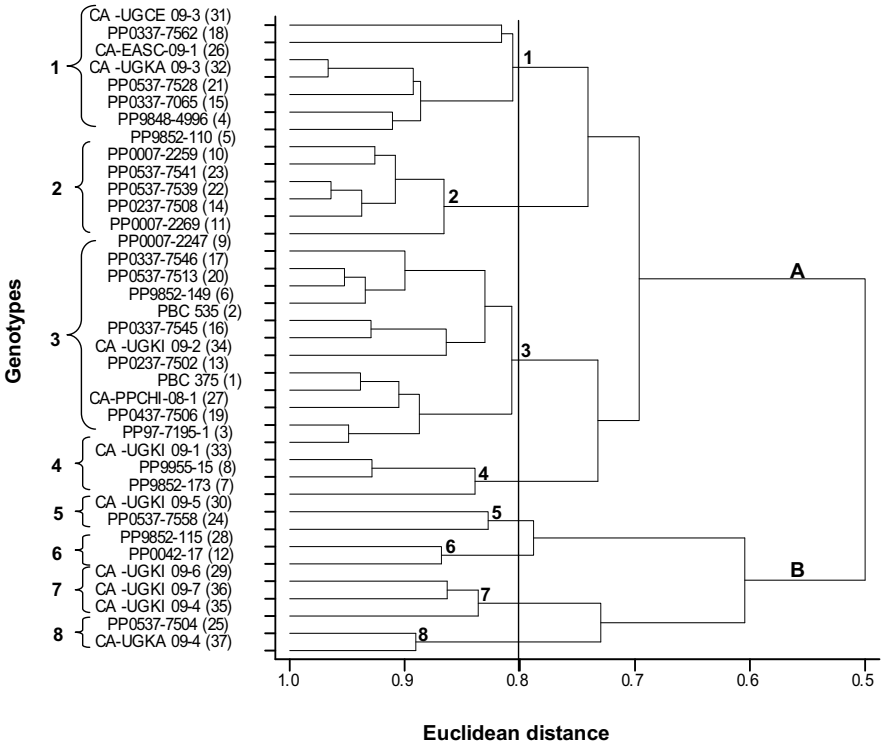

Fig. 3 Dendrogram generated by hierarchical cluster analysis showing the interrelationships observed among the characterized chilli pepper genotypes using 28 qualitative traits. In brackets are genotype codes. Euclidean Distance = Coefficient of similarity.

terized including; stem pubescence type, plant growth habit, leaf surface, leaf pubescence, leaf pubescence type, stigma exsertion, pedicel position, fruit anthocyanin spots/stripes, immature fruit colour intensity, fruit shape at pedicel attachment and fruit surface (**Table 8**).

DISCUSSION AND CONCLUSION

The narrow diversity of pepper types available for commercial production in Uganda poses a challenge to production. In order to address the challenges faced by commercial farmers, this research sought to assemble and characterize improved genotypes alongside local types with the view of establishing the diversity among them for a breeding program for *Capsicum* (AVRDC 1990; Bosland and Votava 2012). Selected local and exotic pepper genotypes from Uganda, AVRDC and China were characterized using recommended qualitative and quantitative morphological descriptors (IPGRI *et al*. 1995; Engle 2001).

Most of the qualitative traits analyzed were found variable and could be used to discriminate among genotypes. These traits included: fruit colour, size and shape; nodal anthocyanin, stem pubescence type and density, pedicel position and stigma exsertion. All quantitative traits were also found to differ highly significantly among genotypes with the exception of primary branch numbers. Variations in growth, quality and yield traits have been reported among pepper genotypes elsewhere (Denton *et al*. 2000; Manju and Sreelathakumary 2002; Adetula and Olakojo 2006; Thul *et al*. 2009; Sharma *et al*. 2010). In particular, high coefficients of variation were obtained for fruit weight (22.2%) and number of fruit per plant (36.3%) implying higher magnitude of variability among genotypes for these traits (Nandadevi and Hosaman 2003; Rodríguez *et al*. 2008; Manyasa *et al*. 2009; Sharma *et al*. 2010). Results of PCA further supported occurrence of diversity recorded from ANOVA. Interpretation of the PCA based on the first two principal components explained the greater part (55.4%) of the total variability (Wuensch 2010; Anonymous 2010), with PC1 contributing 28.16% and PC2 27.23%. These results are comparable with the findings of Madu and Uguru (2006) who found the first two components accounting for 54.6% of total variance in hot pepper.

High levels of similarity were also recorded from PCA bi-plot among genotypes that clustered together as demonstrated by three groups of local genotypes (35, 30, 34, 37), (26, 32), (36, 33, 29), two groups of exotic genotypes and a group of genotypes around the centre (22 exotic and 3 local genotypes). None of the genotypes in these groups can be used to improve the other. Nevertheless, genotypes 26, 32, 35, 19, 8, and 27 that isolated more from the rest were considerably more diverse from the rest and could make good candidates for pepper improvement in their respective superior traits. Specifically, genotypes 32 and 26 that were short and early-maturing could be good sources of genes for earliness while genotypes 35, 30, 34, 37 35 that were tall with wide canopy and stems may be useful sources of genes for tallness, many branch numbers and bigger stems that could enhance resistance to lodging in susceptible genotypes such as 26 and 32, which exhibited weak stems.

Genotype 27 produced relatively bigger (width) and heavier fruit, with thicker fruit walls than the other genotypes probably explaining why it scattered far from all the genotypes in its category. Together with genotype 18 and 19, 27 also produced fewer secondary branch numbers and hence fewer numbers of fruits per plant but of a bigger size. These genotypes could thus provide good sources of genes for bigger fruits which is an essential market quality (AVRDC 1989; Bozokalfa and Kilic 2010). These genotypes would, however, need to be improved for production of high numbers of fruit per plant in order to enhance yield. The local commercial genotype 31 may be a prime candidate for the latter trait since it produced the highest number of fruits per plant and secondary branch numbers although its small fruit size may lower productivity. Fruit weight and number of fruits per plant are major traits that directly contribute to yield (Hanson *et al*. 2007; Rodríguez *et al*. 2008; Bozokalfa and Kilic 2010). Combining both traits into a single genotype would improve hot pepper yields in Uganda although this may prove challenging because big fruited genotypes have been reported to abort flowers in order to facilitate other fruits to reach maturity while the small fruited genotypes compensate for yields by having several fruits per cluster (Rodríguez *et al*. 2008), a quality that was also observed among the big fruited genotypes in this study, which also possessed fewer fruits per plant.

In the bi-plot, genotypes were further clustered regardless of place of origin suggesting some level of relatedness as in the case of local genotypes 29, 33 and 36 that clustered with most AVRDC genotypes around the centre of the bi-plot. Similar observations were reported by Madu and Uguru (2006) in hot pepper in Nigeria. Nevertheless, a higher level of diversity was observed among local genotypes than exotic genotypes as evidenced by most exotic genotypes clustering together while clusters of local genotypes were far apart (**Fig. 1**). Phenotypic relatedness was also evident in results of the cluster analyses using quantitative and qualitative traits, with two major clusters being formed for all genotypes evaluated. While this may probably be attributed to the fact that the genotypes belong to the same species (*Capsicum annuum*), their origination from the same ancestral gene pool cannot be totally rejected especially since close genotypic relatedness is further evidenced by the narrow range of coefficient of similarity 0.889-0.996 for genotype clusters (quantitative traits) and 0.806-0.968 (qualitative traits). Even though collection sites were not considered during clustering, the relatedness and closeness among genotypes also appeared not to be influenced by geographical origin as observed in the bi-plot. Votava *et al*. (2005) had a similar observation when they studied the relationship among *C. annuum* genotypes from northern New Mexico, Colorado and Mexico using RAPD markers.

Capsicum annuum is believed to have originated from Central and South America and spread to Europe and other parts of the world including Asia and Africa where the germplasm characterized in this study was collected (Bosland 1996; Ochoa-Alejo and Ramirez-Malagon 2001; Terry and Boyhan 2006; Bosland and Votava 2012). However, the observed and/or detected diversity could have arisen from pepper germplasm improvement and systematic farmer selection for desirable fruit traits. The lowest diversity for quantitative traits was observed in local genotypes 29 and 36 that were characterized by similarity in growth habit, fruit shape and size although they differed in fruit position and colour, with genotype 29 being orange with erect fruits while genotype 36 was red with pendant fruits. These two genotypes were sourced from Chahi and Nyakabande subcounties in Kisoro District, whose close proximity may have facilitated possible gene flow (Waines and Hegde 2003; Portis *et al*. 2006; Thul *et al*. 2009). On the other hand, the low diversity for qualitative traits observed between local genotypes 26 (from the East African Seed Company) and 32 (local genotype from Kasese) could have simply originated from the same genetic source but developed along different morphological lines due to outcrossing with other related genotypes. Local genotypes were characterized mostly by small fruit size, late-maturity and tallness and must have experienced limited selection or improvement compared to the introduced genotypes that were early-maturing and had bigger fruit sizes.

This study has, thus, revealed morphological diversity among the collections of exotic and local pepper germplasm characterized. While the higher diversity among local genotypes compared with exotic genotypes may be attributed to different directions of artificial selection, fewer local compared with the higher numbers of exotic genotypes characterized might have contributed to this observation (Oyama *et al*. 2006). However, most genotypes were closely related apart from a few that were at the extremes such as commercial local genotype 31 and the Chinese seed company 27. This could possibly be attributed to their close genetic background and narrow genetic base due to the small sample analysed. The low within-group genetic diversity may further be attributed to homozygous and true breeding cultivars resulting from continued inbreeding for uniformity and selection for desirable traits (Bisognin *et al*. 2002; Gichimu *et al*. 2009). Molecular markers may be useful in discriminating among these types and also confirm the phenotypic diversity observed. From this study, the potential of local and improved *Capsicum* pepper germplasm for improvement of quality and productivity of Ugandan pepper was revealed. The preferred local commercial genotype 31 (CA-UGCE 09-3) exhibited high productivity with respect to fruit numbers but will need to be improved for fruit size. Exotic genotypes 19 (PP0437-7506), 8 (PP9955-15) and 27 (CA-EASC-09-1) that produced big fruits will be useful sources of genes for improving the fruit size in this and other local commercial varieties in order to enhance their market acceptability. The genotypes characterized in this study were also assessed for growth, yield, quality and disease resistance. Superior types were used in crossing to develop improved hybrids.

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